

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number:

10/567,537

Source:

IFWP

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4/10/07

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IFWQ

RAW SEQUENCE LISTING

DATE: 04/10/2007

PATENT APPLICATION: US/10/567,537

TIME: 12:02:03

Input Set : A:\HNV-9001 seq listingt.txt

Output Set: N:\CRF4\04102007\J567537.raw

3 <110> APPLICANT: TSAI, LI-HUEI
 4 KOSIK, KENNETH S.
 6 <120> TITLE OF INVENTION: siRNA BASED METHODS FOR TREATING ALZHEIMER'S DISEASE
 8 <130> FILE REFERENCE: HNV-090.01
 10 <140> CURRENT APPLICATION NUMBER: 10/567,537
 C--> 11 <141> CURRENT FILING DATE: 2006-02-07
 13 <150> PRIOR APPLICATION NUMBER: PCT/US04/25633
 14 <151> PRIOR FILING DATE: 2004-08-09
 16 <150> PRIOR APPLICATION NUMBER: 60/493,614
 17 <151> PRIOR FILING DATE: 2003-08-08
 19 <160> NUMBER OF SEQ ID NOS: 20
 21 <170> SOFTWARE: PatentIn Ver. 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1506
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (1)..(1506)
 32 <400> SEQUENCE: 1
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 34 Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 35 1 5 10 15
 37 ctg cct gcc cac ggc acc cag cac ggc atc cgg ctg ccc ctg cgc agc 96
 38 Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
 39 20 25 30
 41 ggc ctg ggg ggc gcc ccc ctg ggg ctg cgg ctg ccc cgg gag acc gac 144
 42 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 43 35 40 45
 45 gaa gag ccc gag gag ccc ggc cgg agg ggc agc ttt gtg gag atg gtg 192
 46 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 47 50 55 60
 49 gac aac ctg agg ggc aag tcg ggg cag ggc tac tac gtg gag atg acc 240
 50 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 51 65 70 75 80
 53 gtg ggc agc ccc ccg cag acg ctc aac atc ctg gtg gat aca ggc agc 288
 54 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 55 85 90 95
 57 agt aac ttt gca gtg ggt gct gcc ccc cac ccc ttc ctg cat cgc tac 336
 58 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 59 100 105 110
 61 tac cag agg cag ctg tcc agc aca tac cgg gac ctc cgg aag ggt gtg 384
 62 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val

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63          115          120          125
65 tat gtg ccc tac acc cag ggc aag tgg gaa ggg gag ctg ggc acc gac 432
66 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
67          130          135          140
69 ctg gta agc atc ccc cat ggc ccc aac gtc act gtg cgt gcc aac att 480
70 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
71 145          150          155          160
73 gct gcc atc act gaa tca gac aag ttc ttc atc aac ggc tcc aac tgg 528
74 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
75          165          170          175
77 gaa ggc atc ctg ggg ctg gcc tat gct gag att gcc agg cct gac gac 576
78 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
79          180          185          190
81 tcc ctg gag cct ttc ttt gac tct ctg gta aag cag acc cac gtt ccc 624
82 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
83          195          200          205
85 aac ctc ttc tcc ctg cag ctt tgt ggt gct ggc ttc ccc ctc aac cag 672
86 Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
87          210          215          220
89 tct gaa gtg ctg gcc tct gtc gga ggg agc atg atc att gga ggt atc 720
90 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
91 225          230          235          240
93 gac cac tcg ctg tac aca ggc agt ctc tgg tat aca ccc atc cgg cgg 768
94 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
95          245          250          255
97 gag tgg tat tat gag gtg atc att gtg cgg gtg gag atc aat gga cag 816
98 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
99          260          265          270
101 gat ctg aaa atg gac tgc aag gag tac aac tat gac aag agc att gtg 864
102 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
103          275          280          285
105 gac agt ggc acc acc aac ctt cgt ttg ccc aag aaa gtg ttt gaa gct 912
106 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
107          290          295          300
109 gca gtc aaa tcc atc aag gca gcc tcc tcc acg gag aag ttc cct gat 960
110 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
111 305          310          315          320
113 ggt ttc tgg cta gga gag cag ctg gtg tgc tgg caa gca ggc acc acc 1008
114 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
115          325          330          335
117 cct tgg aac att ttc cca gtc atc tca ctc tac cta atg ggt gag gtt 1056
118 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
119          340          345          350
121 acc aac cag tcc ttc cgc atc acc atc ctt ccg cag caa tac ctg cgg 1104
122 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
123          355          360          365
125 cca gtg gaa gat gtg gcc acg tcc caa gac gac tgt tac aag ttt gcc 1152
126 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
127          370          375          380

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129 atc tca cag tca tcc acg ggc act gtt atg gga gct gtt atc atg gag 1200
130 ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val ile Met Glu
131 385 390 395 400
133 ggc ttc tac gtt gtc ttt gat cgg gcc cga aaa cga att ggc ttt gct 1248
134 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg ile Gly Phe Ala
135 405 410 415
137 gtc agc gct tgc cat gtg cac gat gag ttc agg acg gca gcg gtg gaa 1296
138 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
139 420 425 430
141 ggc cct ttt gtc acc ttg gac atg gaa gac tgt ggc tac aac att cca 1344
142 Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn ile Pro
143 435 440 445
145 cag aca gat gag tca acc ctc atg acc ata gcc tat gtc atg gct gcc 1392
146 Gln Thr Asp Glu Ser Thr Leu Met Thr ile Ala Tyr Val Met Ala Ala
147 450 455 460
149 atc tgc gcc ctc ttc atg ctg cca ctc tgc ctc atg gtg tgt cag tgg 1440
150 ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
151 465 470 475 480
153 cgc tgc ctc cgc tgc ctg cgc cag cag cat gat gac ttt gct gat gac 1488
154 Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp
155 485 490 495
157 atc tcc ctg ctg aag tga 1506
158 ile Ser Leu Leu Lys
159 500
162 <210> SEQ ID NO: 2
163 <211> LENGTH: 501
164 <212> TYPE: PRT
165 <213> ORGANISM: Homo sapiens
167 <400> SEQUENCE: 2
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169 1 5 10 15
171 Leu Pro Ala His Gly Thr Gln His Gly ile Arg Leu Pro Leu Arg Ser
172 20 25 30
174 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
175 35 40 45
177 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
178 50 55 60
180 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
181 65 70 75 80
183 Val Gly Ser Pro Pro Gln Thr Leu Asn ile Leu Val Asp Thr Gly Ser
184 85 90 95
186 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
187 100 105 110
189 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
190 115 120 125
192 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
193 130 135 140
195 Leu Val Ser ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn ile
196 145 150 155 160

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198 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
199          165          170          175
201 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
202          180          185          190
204 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
205          195          200          205
207 Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
208          210          215          220
210 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
211 225          230          235          240
213 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
214          245          250          255
216 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
217          260          265          270
219 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
220          275          280          285
222 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
223          290          295          300
225 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
226 305          310          315          320
228 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
229          325          330          335
231 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
232          340          345          350
234 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
235          355          360          365
237 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
238          370          375          380
240 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
241 385          390          395          400
243 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
244          405          410          415
246 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
247          420          425          430
249 Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
250          435          440          445
252 Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
253          450          455          460
255 Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
256 465          470          475          480
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259          485          490          495
261 Ile Ser Leu Leu Lys
262          500
266 <210> SEQ ID NO: 3
267 <211> LENGTH: 19
268 <212> TYPE: DNA
269 <213> ORGANISM: Homo sapiens
271 <400> SEQUENCE: 3

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Input Set : A:\HNV-9001 seq listingt.txt

Output Set: N:\CRF4\04102007\J567537.raw

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272 gctttgtgga gatggtgga 19
275 <210> SEQ ID NO: 4
276 <211> LENGTH: 19
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278 <213> ORGANISM: Mus musculus
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285 <211> LENGTH: 19
286 <212> TYPE: DNA
287 <213> ORGANISM: Rattus sp.
289 <400> SEQUENCE: 5
290 gctttgtgga gatggtgga 19
293 <210> SEQ ID NO: 6
294 <211> LENGTH: 19
295 <212> TYPE: DNA
296 <213> ORGANISM: Mus musculus
298 <400> SEQUENCE: 6
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302 <210> SEQ ID NO: 7
303 <211> LENGTH: 19
304 <212> TYPE: DNA
305 <213> ORGANISM: Homo sapiens
307 <400> SEQUENCE: 7
308 acttcttggc catggtaga 19
311 <210> SEQ ID NO: 8
312 <211> LENGTH: 19
313 <212> TYPE: DNA
314 <213> ORGANISM: Homo sapiens
316 <400> SEQUENCE: 8
317 gacgtcaac atcctggtg 19
320 <210> SEQ ID NO: 9
321 <211> LENGTH: 19
322 <212> TYPE: DNA
323 <213> ORGANISM: Mus musculus
325 <400> SEQUENCE: 9
326 gacgtcaac atcctggtg 19
329 <210> SEQ ID NO: 10
330 <211> LENGTH: 19
331 <212> TYPE: DNA
332 <213> ORGANISM: Rattus sp.
334 <400> SEQUENCE: 10
335 gacgtcaac atcctggtg 19
338 <210> SEQ ID NO: 11
339 <211> LENGTH: 19
340 <212> TYPE: DNA
342 <213> ORGANISM: Mus musculus
344 <400> SEQUENCE: 11
345 gaaggtacag attcttgtg 19

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/567,537

DATE: 04/10/2007

TIME: 12:02:04

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Output Set: N:\CRF4\04102007\J567537.raw

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